Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application. Please amend claim 67.

Listing of Claims:

1. - 62. (Cancelled)

63. (Previously Presented) A fragment complementation system, said system comprising:

a first oligopeptide comprising an N-terminal fragment of a Class A β-lactamase protein covalently bonded through a first Class A β-lactamase protein break-point to a first interactor domain; and

a second oligopeptide comprising a C-terminal fragment of a Class A β-lactamase protein covalently bonded through a second Class A β-lactamase protein break-point to a second interactor domain,

wherein upon binding of said first interactor domain with said second interactor domain, said N-terminal fragment and said C-terminal fragment functionally reconstitute to form the Class A β-lactamase protein.

64. (Previously Presented) The fragment complementation system of claim 63, wherein said first oligopeptide and said second oligopeptide comprise a signal peptide that translocates said first oligopeptide and said second oligopeptide through the plasma membrane of the host cell in which said first oligopeptide and said second oligopeptide are expressed.

65. (Previously Presented) The fragment complementation system of claim 63, wherein said first Class A β-lactamase protein break-point and said second Class A β-lactamase protein break-point are within 10 amino acids in either direction from a junction between 2 amino acid residues, wherein said 2 amino acid residues are within a loop between elements of secondary structure.

66. (Previously Presented) The fragment complementation system of claim 65, wherein said Class A β-lactamase protein comprises SEQ ID NO:2.

67. (Currently Amended) The fragment complementation system of claim 66, wherein said first β-lactamase protein break-point and said second β-lactamase protein break-point are within 10 amino acids in either direction from a junction between 2 amino acid residues in SEQ ID NO:2 selected from the group consisting of ~~**P174 and N175; E197 and L198; K215 and V26; A227 and G228; and G253 and K254**~~ **P149 and N150, E172 and L173, K190 and V191, A202 and G203, and G228 and K229**.

68. (Previously Presented) The fragment complementation system of claim 63, wherein said fragment complementation system further comprises a first peptide that enhances the functional reconstitution of said N-terminal fragment and said C-terminal fragment in comparison with the identical system without said first peptide, wherein said first peptide is 3-12 amino acids in length.

69. (Previously Presented) The fragment complementation system of claim 68, wherein said first peptide is 3 amino acids in length.

70. (Previously Presented) The fragment complementation system of claim 69, wherein said first peptide is covalently bonded to the active site of a thioredoxin protein, wherein the sequence of said first peptide is GRE.

71. (Previously Presented) The fragment complementation system of claim 63, wherein

said first oligopeptide further comprises a first polypeptide linker that separates the N-terminal fragment of a Class A β-lactamase protein from the first interactor domain, wherein said first polypeptide linker is 3-30 amino acids in length; and

said second oligopeptide further comprises a second polypeptide linker that separates the C-terminal fragment of a Class A β-lactamase protein from the second interactor domain, wherein said second polypeptide linker is 3-30 amino acids in length.

72. (Previously Presented) The fragment complementation system of claim 71, wherein

said first oligopeptide further comprises a first complementation enhancement peptide fused between the N-terminal fragment of a Class A β-lactamase protein and the first polypeptide linker; and

said second oligopeptide further comprises a second complementation enhancement peptide fused between the C-terminal fragment of a Class A β-lactamase protein and the second polypeptide linker

73. (Previously Presented) The fragment complementation system of claim 72, wherein

the sequence of said first complementation enhancement peptide is selected from the group consisting of HSE, GRE, EKR, and NGR, and

the sequence of said second complementation enhancement peptide is selected from the group consisting of REQ, QGN, DGR, GRR and GNS.

74. (Previously Presented) The fragment complementation system of claim 73, wherein

if the sequence of said first complementation enhancement peptide is HSE, then the sequence of said second complementation enhancement peptide is REQ;

if the sequence of said first complementation enhancement peptide is NGR, then the sequence of said second complementation enhancement peptide is selected from the group consisting of REQ and GNS;

if the sequence of said first complementation enhancement peptide is GRE, then the sequence of said second complementation enhancement peptide is DGR; and

if the sequence of said first complementation enhancement peptide is EKR, then the sequence of said second complementation enhancement peptide is GRR.